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(54) Title: LYCOPENE CYCLASE GENE

(57) Abstract

A purified and isolated DNA sequence encoding lycopene cyclase.

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LYCOPENE CYCLASE GENE

TECHNICAL FIELD

The present invention relates to the isolation of the DNA sequence for lycopene cyclase, and its regulatory sequences, and the use of the DNA sequence or regulatory sequences in preparing native and transgenic organisms in which the production of β-carotene and other carotenoids is controlled by the presence of the DNA sequence or to modify the expression of native genes.

BACKGROUND OF THE INVENTION

Carotenoids are the largest class of pigments in nature. They are synthesized *de novo* only in photosynthetic organisms and in several bacteria and fungi. Their essential function in plants is that of protecting against photo-oxidative damage sensitized by chlorophyll in the photosynthetic apparatus (Koyama, 1991; Siefermann-Harms, 1987), but they play a variety of other roles as well. They serve as accessory pigments in light-harvesting for photosynthesis and are integral components of photosynthetic reaction centers. Carotenoids are involved in the thermal dissipation of light energy captured by the light-harvesting antenna (Demmig-Adams et al., 1992), are substrates for the biosynthesis of the plant growth regulator abscisic acid (Zeevaart et al., 1988; Rock et al., 1991), and are the coloring agents of many flowers, fruits and animals. Certain cyclic carotenoids, including β-carotene, are precursors of vitamin A in human and animal diets and are of current interest as anticancer agents (Mathews-Roth et al., 1991; Palozza et al., 1992).

The generally accepted pathway of carotenoid biosynthesis in plants (Britton, 1988) begins with the head-to-head condensation of two molecules of the soluble 20 carbon compound geranylgeranyl pyrophosphate to give the colorless, membrane-bound carotenoid phytoene (Figure 1). This two-step reaction in plants and cyanobacteria is catalyzed by a single, soluble enzyme: phytoene synthase (Dogbo, 1988; Chamovitz et al.; Linden, 1991; Pecker et al., 1992). Two sequential desaturations of phytoene result in the formation of first phytofluene and then ζ-carotene. Both of these reactions are carried out by a single enzyme in plants and cyanobacteria - phytoene desaturase (Linden et al., 1991; Pecker et al., 1992; Hugueney et al., 1992). This enzyme, and enzymes catalyzing subsequent steps in the pathway, are believed to be membrane-bound (Bramley, 1985). Two additional desaturations yield the symmetrical red carotenoid pigment lycopene, which is then converted to the yellow β-carotene via cyclization reactions at each end of the molecule (Figure 1). Subsequent reactions in the pathway involve the addition of various oxygen functions to form the xanthophylls or oxygenated carotenoids.

Despite many efforts, few of the enzymes or genes of the carotenoid biosynthetic pathway have been identified and isolated in oxygenic photosynthetic organisms. The difficulties of preserving catalytic activity during purification of these largely membrane-bound enzymes have proven formidable, and the unavailability of labelled substrates for enzyme assay is also an obstacle.

Genes for the complete carotenoid biosynthetic pathways in the photosynthetic bacterium *Rhodobacter capsulatus* (Armstrong et al., 1989) and the nonphotosynthetic bacteria *Erwinia uredovora* (Misawa et

al., 1990) and *Erwinia herbicola* (Hundle et al., 1993) have been cloned and sequenced. It was initially thought that such genes would provide molecular probes enabling the identification of homologous genes in oxygen-evolving photosynthetic organisms (cyanobacteria, algae, and plants). However, this approach has not proven fruitful because the *Rhodobacter* and *Erwinia* gene products bear little or no resemblance to the corresponding enzymes in oxygenic photosynthetic organisms (Pecker et al, 1992; Armstrong, 1994).

Two genes, those for phytoene synthase (Chamovitz et al., 1992; Ray et al., 1987) and phytoene desaturase (Pecker et al., 1992, 1993; Hugueney et al., 1992), have now been cloned from oxygenic photosynthetic organisms using other approaches. There is high conservation in the amino acid sequences of the cyanobacterial phytoene desaturase and the gene product of eukaryotic algae and higher plants (Pecker et al., 1992, 1993), but very little resemblance to the known bacterial or fungal phytoene desaturases.

The transformable cyanobacterium *Synechococcus* sp. PCC7942 is used herein as a model organism to study the carotenoid biosynthetic pathway in oxygen-evolving photosynthetic organisms. Applicants earlier cloned genes for phytoene synthase (*psy*, formerly called *pys*) and phytoene desaturase (*pds*) in this organism (Chamovitz et al., 1991; Chamovitz et al., 1992) and subsequently identified, cloned and sequenced plant and algal genes using the cyanobacterial genes as probes (Pecker et al., 1992, Chamovitz et al., 1991; Pecker et al., 1993; Bartley et al., 1991). The gene *pds* was identified with the aid of a bleaching herbicide, norflurazon, that specifically inhibits the desaturation of phytoene by interacting with the enzyme phytoene desaturase (Sandmann, 1989a). It was reasoned

that a point mutation in the gene encoding the enzyme, leading to an amino acid substitution in the polypeptide, could confer resistance to the herbicide. By selecting for chemically-induced mutants which are resistant to norflurazon, and then mapping these mutations by genetic complementation of the resistance in the wild-type strain, applicants located the gene for phytoene desaturase (Chamovitz, 1990; Chamovitz et al., 1991).

It would be useful to be able to modify carotenoid synthesis to improve the nutritional value, pharmacology and appearance of plants. In so doing there are considerations which favor utilizing native genes where possible. In order to directly incorporate bacterial-origin genes in plants, the genes may require further modification to be able to be used, for example, in regulating the photosynthetic pathway. Further, bioengineered plants require regulatory approval prior to release to the environment. The regulatory process is more difficult if foreign genes are present. It would be more efficient to utilize the native genes, or DNA sequences, in controlling, for example, the β-carotene pathway.

Further, it would be useful to have available crops that are tolerant to herbicides that target the action of lycopene cyclase. Herbicides that target the carotenoid pathway may be of low toxicity since this pathway does not occur in humans, animals or insects. Further, plants that are herbicide tolerant at two loci within the carotenoid pathway would offer the potential for alternating applications of two herbicides thereby minimizing the appearance and selection of herbicide tolerant weed species.

SUMMARY OF THE INVENTION AND ADVANTAGES

According to the present invention, a DNA sequence encoding lycopene cyclase, has been purified and isolated. Both the genomic DNA sequence (SEQ ID No:1) from a cyanobacteria and cDNA sequence from tobacco (SEQ ID No:4) and tomato (SEQ ID No:5) have been purified and isolated.

The present invention further includes the method of manipulating the expression of native genes thereby not requiring the presence of foreign genes in the organism.

The present invention further includes the method of expressing the biosynthetic pathway from geranylgeranyl pyrophosphate to β-carotene in a suitable host cell, selected from eucaryotic and procaryotic cells, by incorporating the sequences encoding the enzymes controlling the pathway, including the sequence for lycopene cyclase. This method can be used to produce β-carotene in an organism not presently producing β-carotene thereby increasing the nutritional value, pharmacology or visual appearance value of the organism.

The present invention further includes the method for regulating expression of lycopene cyclase in transgenic organisms, constitutively or in a tissue-specific manner, to control the content of β-carotene or other carotenoids following in the biosynthetic pathway.

The present invention also includes a transgenic organism wherein the anti-sense expression of the sequence for lycopene cyclase, is incorporated into the genomic DNA thereby inhibiting the synthesis of lycopene cyclase and accumulating the red pigment lycopene. This method can provide a red color to an organism not previously red or deepen the red appearance of a presently red organism.

Finally, the present invention also includes the construction of transgenic plants that are resistant to the action of herbicides such as the herbicide MPTA and other related compounds of the trialkylamines and other herbicides which interact with the lycopene cyclase enzyme.

BRIEF DESCRIPTION OF THE DRAWINGS

Other advantages of the present invention will be readily appreciated as the same becomes better understood by reference to the following detailed description when considered in connection with the accompanying drawings wherein:

FIGURE 1 is a diagram of the carotenoid biosynthetic pathway in cyanobacteria and plants (IPP = isopentenyl pyrophosphate; GPP = geranyl pyrophosphate; FPP = farnesyl pyrophosphate; GGPP = geranylgeranyl pyrophosphate; PPPP = prephytoene pyrophosphate);

FIGURE 2 is a photograph of petri dishes showing MPTA-resistance in mutants (numbered) and two wild-type strains (C and S) of the cyanobacterium *Synechococcus* sp. PCC 7942, the wild-type strain indicated by the letter C was the parent strain from which the mutants were derived, the concentration of MPTA, in micromolar, is given in the upper right corner of each petri dish, and each strain was spotted in several places on each petri dish because of a modest positional influence on survival;

FIGURE 3 is a diagram representing a map showing the mutation site of $MPTA^r$-5 (mutant 5) wherein various subfragment of the 4.6 kB EcoRI-BamHI genomic fragments (indicated below the restriction map) were cloned in the vector pBluescript KS' and transfected to cells of the wild-type strain of *Synechococcus* sp. PCC7942,

and their ability to confer herbicide-resistance (indicated by +) was established by plating the transformants on MPTA containing medium (B=BamHI; C=ClaI; E=EcoRI; K=KpnI; H=HindIII; P=PstI; S=SalI; X=XbaI), rev = reverse orientation;

FIGURE 4 is a diagram representing a map showing that lycopene cyclase activity maps to a region that includes the MPTA resistance lesion(s), abbreviations are as in Figure 3;

FIGURE 5 is a diagram of the construction of plasmids pLCYB-M5XE and pLCYB-M5PPF wherein the putative localization of the *lcy* (*crtL*) gene in mutant number 5 is based on expression experiments (see Figure 4);

FIGURE 6 is a graph presenting the HPLC analysis of carotenoid pigments extracted from cells of a lycopene-accumulating strain of *E. coli* (panel A), a lycopene-accumulating strain of *E. coli* containing pLCYB-M5XE (panel B), a lycopene-accumulating strain of *E. coli* containing pLCYB-M5XE in the presence of MPTA (panel C) wherein the effect of treatment of the *E. coli* cells with 100 mM MPTA is shown, and the absorbance spectra of peaks 1, 3 and 5 are shown in the lower panel {(- - -) peak 1 is lycopene; (———) peak 3 is γ-carotene; (.....) peak 5 is β-carotene};

FIGURE 7 is a diagram showing the identification of a mutation for MPTA resistance within the promoter region upstream of the lycopene cyclase gene; and

FIGURE 8 is a diagram showing a dinucleotide-binding motif at the amino terminus of LCY indicating that FAD is utilized by lycopene cyclase (a is acidic: D or E, p is polar or charged: D,E,K,R,H,S,T,Q,N, s is small or hydrophobic: A,I,L,V,M,C, and * is any amino acid).

DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENT

The present invention consists of a DNA sequence that encodes the enzyme lycopene cyclase (LCY) as best shown in SEQ ID No:1, SEQ ID No:4 and SEQ ID No:5. The present invention further can include at least one additional DNA sequence flanking the DNA sequence as best shown in SEQ ID No:1. This flanking sequence can be a promoter.

The sequence can be the gene, and which has been purified, isolated and cloned from a cyanobacteria (SEQ ID No:1). The sequence also includes cDNA and which has been isolated for tobacco (SEQ ID No:4) and tomato (SEQ ID No:5) for example.

The sequence for lycopene cyclase can either be the wild type or can be modified by point mutations, deletions or insertions such that the resulting sequence is altered imparting herbicide resistance. The modification can be in either the DNA sequence that encodes the enzyme lycopene cyclase (LCY) or in the flanking sequence. A sequence consisting of a modified DNA sequence in the promoter region of the gene for lycopene cyclase conferring resistance to MPTA was also purified, isolated, cloned and sequenced in the practice of the present invention (Figures 2 and 7).

Vectors carrying the DNA sequences as set forth above can also be prepared in the practice of the present invention using methods set forth in the Methods section hereinbelow. Host cells, wherein the host cell is selected from the group of eucaryotic and procaryotic cells which can be transformed with these vectors, can also be prepared in the practice of the present invention. The host cells can be *E. coli*, cyanobacteria such as *Synechococcus* PCC7942 and *Synechocystis* PCC6803, alga and plant cells. Suitable host cells include a carotenogenic organism if only the sequence for lycopene cyclase is used or cells that

contain phytoene, the precursor for *pds* or *crtI* gene products and are host cells which can be transformed by the vector being used.

In the practice of the present invention, transgenic organisms can be constructed which include the DNA sequences as set forth hereinabove that are incorporated into the genomic DNA (Bird et al, 1991; Bramley et al, 1992; Misawa et al, 1994b; Misawa et al, 1994a). The incorporation of these sequences can allow the controlling of carotenoid biosynthesis, content, composition or amount in bacteria, algae, and plants. These transgenic organisms can be constructed to incorporate sequences which allow over-production of lycopene cyclase (Cunningham et al, 1993, 1994), i.e. production over the amount normally present in a cell. In a further embodiment, the transgenic organisms can also incorporate sequences which confer herbicide-resistance thereby producing an herbicide-resistant organism, and in a preferred embodiment resistance to bleaching herbicides of the trialkylamine family including CPTA and MPTA. Other modifications can be introduced to alter regulation of carotenoid biosynthesis.

Transgenic organisms can also be constructed in the present invention wherein the anti-sense expression of the DNA sequence for lycopene cyclase is incorporated into the genomic DNA thereby inhibiting the synthesis of lycopene cyclase and accumulating the red pigment lycopene. Further, in the process of controlling carotenoid biosynthesis, content, composition or amount in bacteria, alga, and plant vectors can be prepared of a DNA sequence consisting of an anti-sense expression of the DNA sequence for lycopene cyclase and these vectors used in transforming cells of bacteria, algae, and plants thereby forming

transgenic organisms (Gray et al, 1994; Hall et al, 1993).

Applicants have recently proposed changing the nomenclature referring to the gene encoding for lycopene cyclase from *lcy* to *crtL* in all species. The *crt* nomenclature originated for the *R. capsulatus* genetic loci required for carotenoid biosynthesis and has been maintained for *Rhodobacter* species, *Erwinia* species and *Thermus thermophilus*. Genetic loci involved in carotenoid biosynthesis in *M. xanthus* have been designated *car* in a parallel nomenclature. In higher plant species the genes were named as abbreviations of the enzyme formed. Applicants have proposed adopting the *crt* nomenclature for higher plants. Accordingly, as used herein *lcy* and *crtL* are equivalent designations. (See Armstrong, 1994, Table I for a comparison of the various nomenclatures.)

Herbicides are generally effective by disrupting selected biochemical pathways. Herbicides that interfere with the carotenoid biosynthetic pathway are particularly effective. These herbicides include a number of substituted triethylamine compounds that inhibit the formation of cyclic carotenoids and result in the accumulation of lycopene in plants, algae, and cyanobacteria (Sandmann et al., 1989b). A particularly effective inhibitor of this class is the compound 2-(4-methylphenoxy)-triethylamine hydrochloride (MPTA) (Yokoyama et al., 1992; Cunningham, 1985). The target site of MPTA and related compounds is believed to be the enzyme lycopene cyclase (Sandmann et al., 1989b).

Applicants have described isolated MPTA-resistant mutants of *Synechococcus* sp. PCC 7942 and cloned a gene that contains one of the mutations (see Figure 7). Expression of this gene in a lycopene-accumulating strain of *E. coli* showed unequivocally that the MPTA-resistance gene encodes lycopene cyclase. DNA

hybridization analysis indicates that the sequence of this gene is conserved among other photosynthetic eukaryotes.

Mutations imparting herbicide resistance can be point mutations, deletions or insertions. The mutations can occur either within the nucleotide sequence of lycopene cyclase, designated *crtL* (originally designated *lcy*) such that the resulting amino acid sequence is altered imparting herbicide resistance or within the flanking sequences of *crtL* such that regulation of the expression of *crtL* is altered imparting herbicide-resistance. An example of the latter mutation is that of mutant 5 as shown in Figure 7. In this mutant, a single base change (base number 1925 in SEQ ID No:1) in the promoter region of *crtL*, 104 base pairs upstream of the initiation codon, changes a C to a T and confers a high degree of herbicide-resistance to cells of *Synechococcus* which contain it (see Figure 2), presumably by greatly increasing biosynthesis of the enzyme.

In cloning the gene for lycopene cyclase, the strategy that was used earlier to identify the gene for phytoene desaturase in *Synechococcus* sp. PCC7942 was used. The rationale for this approach is derived from the assumption that the enzyme lycopene cyclase is the target site of the bleaching herbicide MPTA, and the conjecture that a subtle change in the primary structure of lycopene cyclase could produce an enzyme that was tolerant of MPTA and yet still retain adequate catalytic activity. Applicants did not know, *a priori*, whether the resistant phenotype of a particular mutant was derived from a lesion in the gene for lycopene cyclase. The phenotype selected could as well have been due to an increase in the rate of breakdown or detoxification of the herbicide, or the result of a reduction in herbicide uptake. The functional

expression in *E. coli* of a gene that contains the MPTA-resistance mutation of mutant M^r-5 demonstrated that this gene, originally designated *lcy*, does, in fact, encode the enzyme lycopene cyclase. A number of other MPTA resistance mutations have been mapped to the *lcy* gene. The wild-type gene product (Seq. ID No. 2) and those of these other mutants also function well in *E. coli*.

Lycopene is the primary substrate for the formation of cyclic carotenoids in plants and cyanobacteria. The conversion of lycopene to β-carotene requires that cyclization reactions occur at both ends of the symmetrical lycopene. The present invention demonstrates that a single cyanobacterial enzyme efficiently catalyzes both cyclizations. Accumulation of the monocyclic species γ-carotene in cultures, as described hereinbelow, was not observed in the absence of herbicide, even though a substantial amount of lycopene as well as β-carotene, accumulated in these cells. This observation indicates that any molecule of lycopene which is cyclized at one end has a very high probability of being cyclized at the other end as well. The possibility that lycopene cyclase operates as a homodimeric complex is one explanation for these results.

As part of the isolation and for use in transformation procedures, novel plasmid pLYCB-M5XE was constructed and described herein. Plasmids pLCYB-M5PPF, and pLYCB-M5SP are truncated versions of pLCYB-M5XE and are described herein. The various plasmids were constructed as described in the materials and methods section below.

Using the present invention, it is possible to transform host cells, including *E. coli*, cyanobacteria, algae, and plants, using the appropriate vectors so that they carry either the DNA sequence for lycopene

cyclase or the mutated sequence of DNA for lycopene cyclase that is resistant to MPTA. Such transformed cells allow the regulation of the *lcy* gene and regulation of the catalytic function of LCY.

Applicants observed that no cyclization of ζ-carotene takes place when *lcy* is expressed in cells of *E. coli* that accumulate ζ-carotene. This result implies that the cyclization reactions catalyzed by the *Synechococcus lcy* gene product require that the linear molecule be fully desaturated. It was shown in *Phycomyces* that neurosporene can undergo cyclization only in that half of the molecule which is desaturated to the level of lycopene (Bramley, 1985).

The present invention includes the construction of transgenic organisms that are resistant to MPTA and other herbicides that interfere with the cyclization of lycopene. The agronomical advantage of using an herbicide-resistant crop has been demonstrated in the *Brassica* species, including *B. napus*, where atrazine resistance was introduced by genetic crossing of the crop with a weed of the same genus (Beaversdorf et al., 1980).

The target site of action for MPTA and related compounds has been a matter of some dispute. MPTA was previously shown to induce accumulation of lycopene in grapefruit (Yokoyama, 1982) and to prevent cyclization of lycopene in isolated chloroplasts of *Euglena gracilis* (Cunningham, 1985). Much more work has been done with the structurally-related compound 2-(4-chlorophenylthio)-triethylamine hydrochloride (CPTA) (Sandmann et al., 1989b) with similar results: lycopene accumulation *in vivo*. However, in contrast to the results obtained *in vivo*, CPTA has been reported to exert little or no effect on carotenoid biosynthesis in cell-free systems derived from acetone extracts of tomato plastid (Bucholtz et al., 1977), from *Narcissus*

chromoplasts (Beyer et al., 1980) and from *Capsicum* chromoplasts (Camara et al., 1982). Suggestions have been made that CPTA and related compounds act at the level of gene expression rather than by directly affecting enzyme function (Bucholtz et al., 1977; Fosket et al., 1983; Hsu et al., 1972).

More recent work, using a cell-free system from the cyanobacterium *Aphanocapsa*, indicates that CPTA can be an effective inhibitor of lycopene cyclization *in vitro* and that it inhibits the cyclization reaction in a noncompetitive manner as reviewed by Sandmann et al. (1989b). The lack of inhibition by CPTA observed in many other cell-free systems suggests that the physical integrity of the membrane and/or an ordered structural association of the enzymes of carotenoid biosynthesis are important for effective herbicide action. The fragile nature of the carotenoid biosynthetic machinery in cell free systems is well known (Beyer, 1989).

The finding herein that a mutation in the gene for lycopene cyclase confers resistance to MPTA provides strong evidence that this enzyme is a target site of action for MPTA and related compounds can be made but it is not to be construed as limiting the present invention to this one mode of action. This conclusion is further supported by the observation that MPTA inhibits lycopene cyclase activity in cells of *E. coli* where no authentic cyanobacterial carotenogenic apparatus is presumed. The accumulation of γ-carotene in MPTA treated cells of *E. coli* suggests that the second cyclization step carried out by lycopene cyclase is more sensitive to inhibition by the herbicide. These findings make possible the transformation of crop plants to be MPTA resistant by insertion of any of applicants' many different $MPTA^r$-mutant lycopene cyclase genes. More importantly, the present invention can be used to guide the bioengineering of native plant and

algal genes for resistance to MPTA and other herbicides.

Southern hybridization analysis, using the cyanobacterial *crtL* sequence as a molecular probe, indicates that this gene sequence is conserved with similar DNA sequences in eukaryotic algae, and predicted the feasibility of using *crtL* as a molecular probe to clone lycopene cyclase from algae and higher plants. The isolation of cDNA for lycopene cyclase from tobacco and tomato confirms this utility. It further indicates that transgenic plants carrying the present invention will be functional. The fact that higher plants contain a lycopene cyclase gene that has a sequence similar to *crtL* indicates that, as in the cases of the genes for phytoene synthase and phytoene desaturase, the enzymology of lycopene cyclization in plants is similar to cyanobacteria and distinct from other microorganisms. This implies that *crtL*, by being analogous to the plant homolog, will be functional when expressed in transgenic algae or plants.

In the "plant-type" pathway of carotenoid biosynthesis, applicants have identified genes for all of the steps from geranylgeranyl pyrophosphate to β-carotene except the two desaturations which convert the symmetrical ζ-carotene to lycopene. Cloning of a putative gene for ζ-carotene desaturase has been recently reported (Linden et al., 1993). The desaturation of ζ-carotene in plants and algae is inhibited by a number of experimental bleaching herbicides (Sandmann et al., 1989b), and several of these compounds effectively inhibit the desaturation of ζ-carotene in *Synechococus* PCC7942 (Sandmann et al., 1989b). Applicants' successes in cloning *psy*, *pds*, and the present invention, *crtL* (*lcy*), using techniques known in the art, indicate that the same strategy of mutagenesis and selection of herbicide-resistant

mutants derived under the scope of the invention will enable the cloning of ζ-carotene desaturase with the appropriate inhibitors. From this, the present invention allows the construction of the biosynthetic pathway from geranylgeranyl pyrophosphate to β-carotene in a suitable host cell by incorporating the DNA sequence encoding for *psy*, *pds*, *zds* and *lcy*.

The present invention also includes a transgenic organism wherein the anti-sense expression of the *crtL* gene is incorporated into the genomic DNA thereby inhibiting the synthesis of lycopene cyclase and accumulating the red pigment lycopene. This method can provide a red color to an organism not previously red or deepen the red appearance of a presently red organism. The use of antisense technology to alter gene expression to modify a plant's phenotype has been developed and is now available to those skilled in the art. This technology has been utilized with tomatoes, including the carotenoid biosynthesis pathway (Bramley, 1992; Bird et al., 1991; Hali et al., 1993, United States Patent 5,304,490).

The examples hereinbelow illustrate the methods of isolation, purification and cloning of the respective *crtL* sequences as well as probe/vector construction and use. Further examples demonstrate the use of the vectors to transform suitable host cells such as bacteria, algae and plants, as well as determining the sites of herbicide resistance. Suitable host cells include a carotenogenic organism if only *lcy* is used or cells that contain phytoene, the precursor for *pds* or *crtI* gene products and are host cells which can be transformed by the vector being used.

In summary, the use of the cyanobacterium *Synechococcus* PCC7942 as a model organism for studying the carotenoid biosynthetic pathway has provided findings obtained with this genetically simple and

convenient organism that are broadly applicable to any oxygenic photosynthetic organism (plants, algae, and cyanobacteria). That is, once a carotenoid biosynthesis gene is identified in *Synechococcus*, it is then possible to isolate a gene with sequence similarity from any plant or alga. This has been demonstrated by the applicants' use of the *Synechococcus* gene for phytoene desaturase to clone genes with sequence similarity from plants and algae. Where the plant or algal gene had not been identified, applicants' initial identification of the cyanobacterial gene provided the essential and sufficient tool that enabled identification and cloning of the plant and algal genes for phytoene desaturase. In the present application, identification of a lycopene cyclase gene from *Synechococcus* PCC7942 provides, in the same way, the necessary and sufficient tool to identify and clone algal and plant genes with sequence similarity such as from tomato (SEQ ID No:5) and tobacco (SEQ ID No:4). The *Synechococcus* lycopene cyclase gene, as those for *pds* and *psy* before it, bears little resemblance to the two known bacterial genes from *Erwinia* (Pecker et al, 1992; Armstrong, 1994) or to any other genes in the major databases (GenBank and SwissProt).

Modification of the native genes of plants and algae is now made possible (Bird et al, 1991; Bramley et al, 1992; Misawa et al, 1994b; Misawa et al, 1994a). For example, observations made with the cyanobacterial gene locate the sites of herbicide resistant mutations which can then be used in determining where to alter the native genes for herbicide-resistance. For any new herbicide that appears, resistant mutants are selected to determine what modifications of the amino acid sequence of the enzyme or regulatory DNA Sequences can confer the resistance. The native enzyme of any plant

or regulatory sequence can be changed in the same way, to produce the analogous mutant. In addition, the expression of the genes can be modified and manipulated in a tissue-specific manner and the use of antisense technology (Gray et al, 1994; Hall et al, 1993) with the native genes is also possible.

The above discussion provides a factual basis for the utility of the lycopene cyclase gene. The methods used with and the utility of the present invention can be shown by the following examples.

EXAMPLES

GENERAL METHODS:

Organisms and Growth Conditions. Cultures of *Synechococcus* sp. PCC7942 (*Anacystis nidulans* R2) were grown in BG11 medium at 35°C as described previously (Hirschberg et al., 1987). For selection of MPTA-resistant mutants (MPTA^r) and transformants, cultures were spread on solid BG11 medium containing 1.5% agar (Bacto) and 20 or 30 μM MPTA. The MPTA was added to molten agar at 50°C from a 20 mM stock solution in MeOH immediately before pouring into petri dishes. Where required, kanamycin was incorporated in the BG11 agar plates at a concentration of 10 μg/ml.

Escherichia coli strain XL1-Blue was used as host for genomic libraries of *Synechococcus* in the plasmid vector pBR329K^{25} with kanamycin at 30 μg/ml for selection, and as a host for the plasmid pBluescript II KS$^-$ (Stratagene) and other plasmids with ampicillin at 100 μg/ml and/or chloramphenicol at 50 μg/ml. Cultures of *E. coli* were grown in the dark at 37°C in LB medium (Sambrook et al., 1989).

Selection of MPTA-Resistant Mutants. Cultures of *Synechococcus* were treated with the chemical mutagen ethane methylsulfonate (EMS, Sigma Chemical Company, St. Louis, Missouri) as described previously

(Hirschberg, 1987), and were allowed to grow for 24 hours in liquid culture before selection on BG11 agar plates containing 20 or 30 μM MPTA. Herbicide tolerance in the selected mutants was examined by spotting 3 μl of dilute cultures on a master petri dish of BG11 agar. After two weeks of growth, replicas were made on plates containing different concentrations of MPTA and allowed to grow for two more weeks. Mutants were maintained on BG11 agar plates containing 4 μM MPTA. The MPTA was a generous gift of Dr. Henry Yokoyama, Fruit and Vegetable Chemistry Laboratory, Agricultural Research Service, United States Department of Agriculture, Pasadena, California 91106.

Molecular Cloning. Genomic DNA was extracted (Williams, 1988) from MPTA-resistant *Synechococcus* mutant number five (M^r-5), completely digested with EcoRI, and used to construct a genomic library in the EcoRI site of pBR329K (Chamovitz, 1990). The parent wild-type strain was transformed (Williams, 1988) with DNA of this M^r-5 library, and transformants were selected on BG11 agar plates containing both MPTA (20 or 30 μM) and kanamycin (10 μM). The strategy described in Chamovitz et al. (1990) was employed to recover the plasmid vector, along with flanking genomic DNA. A 2.1 kb EcoRI-SalI genomic DNA fragment, which was recovered in this way, was used as a molecular probe. ^{32}P-labelling was carried out by the random priming method (Feinberg et al., 1983). An 8.5 kb genomic clone, identified by colony hybridization (Sambrook et al., 1989) using this probe, was subcloned in the plasmid pBluescript II KS$^+$ (Stratagene) and was designated pM5EE. Various fragments of this clone were subcloned in the vector pBluescript II KS$^+$ and their ability to transform the wild-type strain of *Synechococcus* sp. PCC7942 to MPTA resistance was

tested. Plasmid DNA minipreps were prepared using the procedure of Del Sal et al. (1988).

Construction of a Lycopene-Accumulating Strain of *E. coli*. To demonstrate activity of lycopene cyclase (LCY) it was essential to modify cells of *Escherichia coli* by genetic engineering so that they will produce lycopene, which is the substrate of the enzyme LCY. Several examples of such an engineering in *E. coli* utilizing genes from *Erwinia* species have been published in the past (Misawa et al., 1990; Hundle et al., 1991; Hundle et al., 1993; Misawa et al., 1991; Sandmann et al., 1990; Schnurr et al., 1991). Briefly, the vector is constructed from a cluster of genes encoding carotenoid biosynthesis enzymes that has been cloned from *Erwinia uredovora* (Misawa et al., 1990). A 2.26 kb BstEII-SnaBI fragment was deleted from the plasmid pCAR (Misawa et al., 1990), and a 3.75 kb Asp718-EcoRI fragment, carrying crtE, crtB and crtI, was subcloned in the EcoRV site of the plasmid vector pACYC184. The resulting vector which has the same insert as the recombinant plasmid designated pCAR-ADE (Misawa et al., 1990) is then used to construct the lycopene-accumulating strain of *E. coli*.

Functional Expression of Lycopene Cyclase in *E. coli*. A 7.2 kb XbaI-EcoRI DNA fragment, containing the MPTA resistance mutation, was cloned in the multiple cloning site of the vector pBluescript II SK$^-$ (Stratagene) and then excised as a SacI-EcoRI fragment. This SacI-EcoRI fragment was then cloned in the IPTG-inducible expression vector pTrcHisB (Invitrogen) and the resulting plasmid, designated pLYCB-M5XE, was used to transform competent cells of the lycopene-accumulating strain of *E. coli* as described hereinabove. Transformed cells were plated on LB agar plates containing ampicillin (100 μg/ml) and chloramphenicol (50 μg/ml), and spread with 10 μl of a

100 mM aqueous solution of isopropylthio-β-D-galactoside (IPTG) one hour before cells were plated.

Carotenoid Pigment Analysis. Cultures of *E. coli* were grown for 18 hours at 37°C in LB medium containing 1 mM IPTG. Bacterial cells from 50 ml of the suspension culture were harvested by centrifugation and carotenoid pigments were extracted by dissolving the pellet in 90% acetone. The carotenoids were analyzed by HPLC on a Spherisorb ODS1 25 cm reverse phase column as previously described (Chamovitz et al., 1992). A Merck/Hitachi HPLC apparatus, consisting of a L6200 pump, L300 multichannel photodetector with D6000 interphase was used, employing an isocratic solvent system of acetonitrile/methanol/isopropanol (85:10.5). The Hitachi DAD Manager software allowed for the simultaneous detection of phytoene and colored carotenoids. Individual carotenoids were identified on the basis of online absorption spectra and typical retention times in comparison to reference standards of lycopene and β-carotene.

Construction and delivery of vectors. Such vectors are known or can be constructed by those skilled in the art and should contain all expression elements necessary to achieve the desired transcription of the sequences. Other beneficial characteristics can also be contained within the vectors such as mechanisms for recovery of the nucleic acids in a different form. Phagemids are a specific example of such beneficial vectors because they can be used either as plasmids or as bacteriophage vectors. Examples of other vectors include viruses such as bacteriophages, baculoviruses and retroviruses, DNA viruses, cosmids, plasmids, liposomes and other recombination vectors. The vectors can also contain elements for use in either procaryotic or eucaryotic host systems. One of ordinary skill in

the art will know which host systems are compatible with a particular vector.

The vectors can be introduced into cells or tissues by any one of a variety of known methods within the art. Such methods can be found generally described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Harbor Laboratory, New York (1992), in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Maryland (1989), Chang et al., *Somatic Gene Therapy*, CRC Press, Ann Arbor, MI (1995), Vega et al., *Gene Targeting*, CRC Press, Ann Arbor, MI (1995) and Gilboa, et al (1986) and include, for example, stable or transient transfection, lipofection, electroporation and infection with recombinant viral vectors. Introduction of nucleic acids by infection offers several advantages over the other listed methods. Higher efficiency can be obtained due to their infectious nature. Moreover, viruses are very specialized and typically infect and propagate in specific cell types. Thus, their natural specificity can be used to target the vectors to specific cell types *in vivo* or within a tissue or mixed culture of cells. Viral vectors can also be modified with specific receptors or ligands to alter target specificity through receptor mediated events.

Other molecular biology methods not expressly set forth. Such methods can be found generally described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Harbor Laboratory, New York (1992), in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Maryland (1989).

EXAMPLES

1. Selection and mapping of MPTA-Resistant Mutants.

Wild-type cells of the cyanobacterium *Synechococcus* sp. PCC7942 did not grow on BG11 agar plates containing more than 2 μM of the bleaching herbicide MPTA. Following mutagenesis of the wild-type strain with EMS and selection for growth on agar plates containing 30 μM MPTA, applicants selected a number of herbicide-tolerant mutants. Mutant number five (M^r-5) exhibited the highest resistance and grew on agar plates containing 50 μM MPTA (Figure 2). This mutant was used for all subsequent experiments described in this application.

The genetic basis of MPTA resistance in M^r-5 was established by transformation experiments. Genomic DNA was extracted from M^r-5, digested with the endonuclease EcoRI and transfected to wild-type cells of *Synechococcus* PCC 7942. The appearance of colonies at high frequency (ca. 10^4 times that for untransformed controls) on agar plates containing 30 μM MPTA demonstrated the genetic character of the resistance to MPTA and indicated that either a single lesion or closely-linked mutations were responsible for the resistance trait.

2. Cloning the MPTA-Resistance Gene.

A genomic library of mutant M^r-5 was constructed in the EcoRI site of the plasmid vector pBR329K (Chamovitz, 1990). DNA of this library was transfected to cells of the wild-type strain as closed circular plasmids, and transformants were selected for growth on BG11 agar plates containing both MPTA and kanamycin. Stable transformation in *Synechococcus* sp. PCC 7942 occurs by integration of the foreign DNA into the bacterial chromosome following homologous recombination (Williams, 1988; Golden, 1988). The doubly-resistant

transformants resulted from a single cross-over event between a plasmid containing genomic DNA with the mutation for MPTA resistance (MPTA), and its homologous sequence in the chromosome. Consequently, the pBR329K plasmid DNA was integrated into the cyanobacterial chromosome adjacent to the MPTA-resistant gene (Figure 2 in the 1990 Chamovitz et al. reference provides detailed explanation).

A portion of the pBR329K vector was recovered, along with a fragment of the adjacent genomic DNA, by digestion of the genomic DNA of a doubly-resistant transformant with either SalI or BamHI endonucleases, followed by DNA ligation reaction, transfection to cells of *E. coli*, and selection for kanamycin resistance (Kan^r). From one such Kan^r-$MPTA^r$ transformant, applicants recovered a 2.1 kb EcoRI-SalI fragment of cyanobacterial genomic DNA. This fragment was used as a molecular probe to screen the original M^r-5 genomic DNA library and identified a plasmid containing an 8.5 kb EcoRI genomic insert. Transfection of this 8.5 kb DNA fragment into cells of the wild-type strain of *Synechococcus* sp. PCC7942 resulted in a high frequency of herbicide-resistant colonies, thus confirming that this fragment contained the mutation conferring $MPTA^r$. A similar test indicated that the mutation was located in a 4.6 kb EcoRI-BamHI fragment, and subsequently it was mapped to a region of 0.2 kb that is delineated by the PstI and SalI restriction sites (Figure 3).

3. The MPTA Resistance Gene Encodes Lycopene Cyclase.

Since MPTA inhibits lycopene cyclization, applicants expected that the MPTA resistance in strain M^r-5 was due to a change in lycopene cyclase, so that mapping the mutation would lead to the gene for this enzyme. Applicants, therefore, tested for the presence

of this gene by expressing cyanobacterial genomic fragments containing the mutation, in cells of *E. coli* that produce lycopene.

The constructed plasmid, as described hereinabove (Misawa et al., 1990), was used which contained genes from the bacterium *E. uredovora* encoding the enzymes GGPP synthase (crtE), phytoene synthase (crtB) and phytoene desaturase (crtI). Cells of *E. coli* carrying this plasmid accumulate lycopene (Figure 6) and produce pink colonies on agar plates.

The plasmid pLCYB-M5XE, which contains a 7.2 kb genomic insert (Figure 5), was introduced into cells of *E. coli* which accumulated lycopene. In the presence or absence of IPTG, colonies and cultures of cells also containing pLCYB-M5XE were yellow in color and contained β-carotene in addition to lycopene as revealed by HPLC analysis (Figure 6). A number of other genomic fragments which contained the mutation, the smallest of which was a 1.5 kb PstI-PstI fragment in the vector pTrcHisB (plasmid pLCYB-M5PPF), gave results similar to those shown in Figure 6 (see also Figure 4). Enzymatic activity was observed with the 1.5 kB *Pst*I fragment cloned in all three frames of the pTrcHis vector and was independent of IPTG induction. Activity was not observed if the fragment was cloned in the reverse orientation. It was concluded that binding of *E. coli* DNA polymerase to the promoter of the vector facilitates recognition and utilization of a cyanobacterial promoter and production of the authentic cyanobacterial enzyme rather than a fusion protein. A truncated version of pLCYB-M5PPF, lacking only the 0.2 kb PstI-SalI portion containing the MPTA-resistant mutation (pLYCB-M5SP), did not sustain lycopene cyclase activity in *E. coli* cells.

DNA sequence analysis revealed a single open reading frame coincident with the mapped location of

lycopene cyclase activity (Figure 7). Applicants concluded that this putative gene, designated as *lcy*, encodes the enzyme lycopene cyclase, and that this single gene product is sufficient to catalyze both cyclization steps required to produce β-carotene from lycopene.

4. Lycopene Cyclase is the Target Site for MPTA inhibition.

Suspension cultures of transformed *E. coli* cells were grown in the presence of 100 μM MPTA in order to examine the interaction between the herbicide and lycopene cyclization activity. HPLC analysis of the carotenoids, shown in Figure 6, indicated that these cells accumulated significant amounts of monocyclic γ-carotene, in addition to lycopene and β-carotene, whereas no γ-carotene was detected in the absence of MPTA. Applicants concluded that MPTA acts directly as an inhibitor of lycopene cyclase.

5. Identification of a mutation for MPTA resistance (Figure 7).

DNA sequence analysis in the region conferring lycopene cyclase activity (Figure 4) revealed a single open reading frame, *lcy*. This open reading frame is of a size to encode a protein of 411 amino acids with a predicted molecular weight of 46,093 g/mol (SEQ ID No:2).

Mutant 5 differs from the wild-type at a single position (position 1925 of SEQ ID No:1), 104 bp upstream of the expected initiation codon of the gene in the promoter region of *lcy* that provides resistance to MPTA. The mutation does not alter the amino acid sequence of the protein encoded by open reading frame 2 (ORF2). The change of a C in the wild-type to a T in M^r-5 produces a 6 base sequence (TACAAT) closer to the consensus for the -10 or Pribnow box of the *E. coli*

promoter region (TATAAT). This T residue in position six of the *E. coli* consensus promoter is highly conserved (96%) while that in the third position is the least conserved base (44%) (Hawley et al, 1983). The mutation to a T in M^r-5 is expected to facilitate DNA strand separation and thereby enhance mRNA production. Overproduction of this message and, consequently, of the enzyme itself, is the most likely explanation for the greatly enhanced MPTA-resistance of mutant 5. This mutant would be expected to be resistant to any other herbicides that act by interfering with lycopene cyclase activity.

Searches of GenBank and SwissProt DNA and protein sequence data banks unearthed no genes or proteins with appreciable sequence similarity to *lcy*. The only resemblance of the predicted amino acid sequence of the protein encoded by *lcy* to other known or reported proteins occurs at the amino terminus of LCY. A nucleotide-binding motif (SEQ ID No:3) is present here in LCY and indicates that this enzyme binds and utilizes cofactor FAD (Figure 8).

6. Isolation and sequences of the *crtL* cDNA in tobacco (SEQ ID No:4) and tomato (SEQ ID No:5).

The tobacco cDNA sequence (SEQ ID No:4) was obtained by screening a leaf cDNA library of *Nicotiana tabacum* (cv. xanthii) using the *crtL* gene (for lycopene cyclase) from *Synechococcus* PCC7942 as a molecular probe. The sequence has been deposited in EMBL/Genbank and has the accession number X81787. The cDNA library is a standard library that was constructed in phage lambda and screened using procedures as generally described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Harbor Laboratory, New York (1992) and in Ausubel et al., *Current Protocols in*

Molecular Biology, John Wiley and Sons, Baltimore, Maryland (1989).

This cDNA sequence (SEQ ID No:4) when carried in a plasmid vector such as described for the *crtL* gene from *Synechococcus* PCC7942, in any of two orientations, can be expressed in *E. coli* cells, produces an active lycopene cyclase enzyme. Its biochemical characteristics are identical to the cyanobacterial enzyme, as described by Cunningham, et al (1993, 1994) and herein above.

The tomato cDNA sequence (SEQ ID No:5) was obtained by screening a leaf cDNA library of *Lycopersicon asculentum* (cv FV36) using the *crtL* gene (for lycopene cyclase) from *Synechococcus* PCC7942 as a molecular probe. The cDNA library is a standard library that was constructed in phage lambda and screened using procedures as generally described in Sambrook et al., *Molecular Cloning: A Laboratory Manual*, Cold Springs Harbor Laboratory, New York (1992) and in Ausubel et al., *Current Protocols in Molecular Biology*, John Wiley and Sons, Baltimore, Maryland (1989).

This cDNA sequence (SEQ ID No:5) when carried in a plasmid vector such as described for the *crtL* gene from *Synechococcus* PCC7942, in any of two orientations, can be expressed in *E. coli* cells, produces an active lycopene cyclase enzyme. Its biochemical characteristics are identical to the cyanobacterial enzyme, as described by Cunningham, et al (1993, 1994) and herein above.

Throughout this application various publications are referenced. Full citations for the referenced publications not cited herein above are listed below. The disclosures of these publications in their entireties are hereby incorporated by reference into

this application in order to more fully describe the state of the art to which this invention pertains.

The invention has been described in an illustrative manner, and it is to be understood that the terminology which has been used is intended to be in the nature of words of description rather than of limitation.

Obviously, many modifications and variations of the present invention are possible in light of the above teachings. It is, therefore, to be understood that within the scope of the appended claims, the invention may be practiced otherwise than as specifically described.

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SEQUENCE LISTING

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(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

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(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 4928 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 2029..3261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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                                                    Val Phe Asp
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  5                  10                  15

CTG GCA CAG CGC GGC TTG AAA GTC CAA GGA CTA TCC CCC GTC GAC CCA      2133
Leu Ala Gln Arg Gly Leu Lys Val Gln Gly Leu Ser Pro Val Asp Pro
 20                  25                  30                  35

TTC CAT CCT TGG GAA AAT ACC TAC GGC ATC TGG GGA CCC GAG CTG GAT      2181
Phe His Pro Trp Glu Asn Thr Tyr Gly Ile Trp Gly Pro Glu Leu Asp
                 40                  45                  50

AGT CTT GGC CTC GAG CAT CTC TTT GGG CAT CGC TGG TCG AAC TGC GTT      2229
Ser Leu Gly Leu Glu His Leu Phe Gly His Arg Trp Ser Asn Cys Val
            55                  60                  65

AGC TAC TTC GGT GAG GCG CCG GTT CAG CAC CAA TAC AAC TAC GGG CTG      2277
Ser Tyr Phe Gly Glu Ala Pro Val Gln His Gln Tyr Asn Tyr Gly Leu
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TTT GAT CGC GCC CAA CTA CAA CAG CAC TGG TTG CGG CAA TGT GAG CAA      2325
Phe Asp Arg Ala Gln Leu Gln Gln His Trp Leu Arg Gln Cys Glu Gln
     85                  90                  95

GGC GGC CTG CAA TGG CAA CTC GGC AAA GCA GCT GCG ATC GCC CAT GAC      2373
Gly Gly Leu Gln Trp Gln Leu Gly Lys Ala Ala Ala Ile Ala His Asp
100                 105                 110                 115

TCC CAC CAT TCC TGC GTT ACG ACA GCA GCA GGG CAG GAG TTA CAG GCG      2421
Ser His His Ser Cys Val Thr Thr Ala Ala Gly Gln Glu Leu Gln Ala
                120                 125                 130

CGG CTG GTT GTC GAT ACG ACT GGG CAC CAA GCG GCT TTT ATC CAG CGA      2469
Arg Leu Val Val Asp Thr Thr Gly His Gln Ala Ala Phe Ile Gln Arg
            135                 140                 145

CCT CAT TCA GAC GCG ATC GCC TAC CAA GCG GCC TAC GGC ATC ATT GGC      2517
Pro His Ser Asp Ala Ile Ala Tyr Gln Ala Ala Tyr Gly Ile Ile Gly
        150                 155                 160

CAG TTT TCG CAG CCG CCG ATC GAG CCC CAT CAG TTT GTG CTG ATG GAC      2565
Gln Phe Ser Gln Pro Pro Ile Glu Pro His Gln Phe Val Leu Met Asp
    165                 170                 175

TAC CGC AGC GAC CAT CTC TCA CCT GAA GAA CGC CAA CTG CCA CCG ACC      2613
Tyr Arg Ser Asp His Leu Ser Pro Glu Glu Arg Gln Leu Pro Pro Thr
180                 185                 190                 195

TTT CTC TAC GCG ATG GAT CTC GGG AAC GAC GTC TAC TTT GTA GAG GAA      2661
Phe Leu Tyr Ala Met Asp Leu Gly Asn Asp Val Tyr Phe Val Glu Glu
                200                 205                 210

ACA TCG CTG GCG GCT TGC CCG GCT ATT CCC TAC GAT CGC CTC AAA CAA      2709
Thr Ser Leu Ala Ala Cys Pro Ala Ile Pro Tyr Asp Arg Leu Lys Gln
            215                 220                 225

CGG CTC TAT CAA CGC TTA GCC ACT CGC GGT GTG ACG GTG CAA GTG ATT      2757
Arg Leu Tyr Gln Arg Leu Ala Thr Arg Gly Val Thr Val Gln Val Ile
        230                 235                 240

CAG CAC GAG GAA TAT TGC CTG TTT CCG ATG AAT TTG CCG CTG CCC GAT      2805
Gln His Glu Glu Tyr Cys Leu Phe Pro Met Asn Leu Pro Leu Pro Asp
    245                 250                 255
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CTC ACT CAG TCA GTG GTT GGC TTT GGG GGG GCG GCC AGT ATG GTG CAT      2853
Leu Thr Gln Ser Val Val Gly Phe Gly Gly Ala Ala Ser Met Val His
260                 265                 270                 275

CCC GCT TCG GGC TAC ATG GTC GGG GCG CTA CTG CGG CGC GCT CCT GAT      2901
Pro Ala Ser Gly Tyr Met Val Gly Ala Leu Leu Arg Arg Ala Pro Asp
                280                 285                 290

CTG GCG AAT GCG ATC GCG GCT GGA CTG AAT GCC AGT TCC AGT CTG ACC      2949
Leu Ala Asn Ala Ile Ala Ala Gly Leu Asn Ala Ser Ser Ser Leu Thr
            295                 300                 305

ACG GCA GAA CTT GCT ACC CAA GCC TGG CGA GGA CTC TGG CCA ACC GAA      2997
Thr Ala Glu Leu Ala Thr Gln Ala Trp Arg Gly Leu Trp Pro Thr Glu
        310                 315                 320

AAA ATT CGC AAG CAC TAC ATC TAC CAA TTC GGC CTC GAA AAG CTG ATG      3045
Lys Ile Arg Lys His Tyr Ile Tyr Gln Phe Gly Leu Glu Lys Leu Met
    325                 330                 335

CGC TTT TCC GAA GCC CAG CTC AAT CAT CAC TTC CAG ACC TTC TTT GGC      3093
Arg Phe Ser Glu Ala Gln Leu Asn His His Phe Gln Thr Phe Phe Gly
340                 345                 350                 355

CTG CCG AAG GAG CAG TGG TAC GGC TTT TTG ACC AAT ACG CTG TCG CTA      3141
Leu Pro Lys Glu Gln Trp Tyr Gly Phe Leu Thr Asn Thr Leu Ser Leu
                360                 365                 370

CCG GAG CTG ATT CAA GCG ATG CTC AGA TTA TTT GCC CAA GCG CCG AAT      3189
Pro Glu Leu Ile Gln Ala Met Leu Arg Leu Phe Ala Gln Ala Pro Asn
            375                 380                 385

GAT GTG CGC TGG GGT CTG ATG GAA CAA CAA GGT CGC GAA TTA CAA CTC      3237
Asp Val Arg Trp Gly Leu Met Glu Gln Gln Gly Arg Glu Leu Gln Leu
        390                 395                 400

TTT TGG CAA GCG ATC GCG GCC CGC TAGCTGCTAA AAACTAGCCG CCCTTGCCAA     3291
Phe Trp Gln Ala Ile Ala Ala Arg
    405                 410

TATCCCGTAA AGTTTTTGAA GCGCTGCTGC ACTTGTTACA GAACCCTAGC GAGCACTTGT    3351

CCTGGTTCCA CTTGAGGATC GATTCCCCCG AGTAATGGCT TCCGAGAACT ACCTCAACCA    3411

TCCCACCTTC GGATTGCTCT ACCAAATCTG CAGCTTTGGG GACAGCAAAG AACTCTTCGC    3471

CACTCTTTAT GCTCAGCGCC TCTTTTTTCT CGTAGCCTTT GATGCTCGGG GAACCCGCTT    3531

TGAGCCAATC GGTCGTAATG AAGCGCGGAT GTTGGTCGAC AACCGTCTGC GCCAGCTGCG    3591

CCGAGATGCC AGTCTGCAGG AATACAACCA GCTGCAGCAA GTCTTCAAAC AAACCTTTCT    3651

GTAGCCAGCT AGGGAGTCAG AGGCAGGCAT GGCCCAAATT GCCGAGCGGT TGGCCAGTCT    3711

CCGATCGCAA CTGCCTCCCA GCGTTCAGCT GATTGCTGTC AGCAAGAACC ATCCCGCTGC    3771

TGCCATCCGA GAAGCCTATG CAGCAGGTCA GCGGCACTTT GGCGAAAATC GGGTCCAAGA    3831

AGCGATCGCT AAGCAAGCGG AACTGACGGA TCTGCCCGAT TTGACTTGGC ATCTGCTGGG    3891

AAAACTGCAG AGCAATAAAG CCCGGAAAGC TGTCGAGCAT TTCGACTGGA TTCATTCAGT    3951

TGATAGCTGG GCCTTGGCTG AACGACTCGA TCGCATTGCG GGAGAGTTGG GGCGATCGCC    4011

CAAGCTTTGC CTCCAGGTGA AGCTCCTGCC TGACCCCAAC AAAGCGGGCT GGGACCCTGC    4071
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TGATTTGCGG GCTGAGTTAC CGCAGCTCAG TCAACTCCAA CAGGTACAAA TCCGCGGCTT 4131

GATGGTGATT GCGCCCCTCG GACTCACCGC CGCTGAGACT CAGGCTCTGT TTGCGCAGGC 4191

TCGCACCTTC GCCGCCGAGT TGCAGCAGCA GGCTCCGCAG CTACGGCTCA CGGAACTCTC 4251

GATGGGCATG TCGAGTGACT GGCCTTTGGC TGTGGCGGAA GGGGCAACTT GGATTCGAGT 4311

CGGAACCCAG TTATTTGGGC CGCGATCGCT GTAATCTTGG CCATAGTTAA CAAACCTTTA 4371

CGTCTTAGAA CTGGCCTAGC AATTGCCATT TCAGGTGCTT TAAGTGGCTT TCCTTAAAAA 4431

AAGCTGAGAT TTGTTCGGTA AAACCAGTCG AAATCTTGCC GTTTGTGCTA TTACTACTGC 4491

GTCTCCATCG ACCTAAGCAG TGCCCTGCGC TCTCGCTAGT GGTCAGCGGA AAAGTGTGGT 4551

GTCGTTGCCC TTGGAGGAAC TGATCGTGTC TTTTGTGAAC CGGATCCGCG ATATCGTCGG 4611

TCTCAATGAG TCGCTGGACT ACGACGAAGA GTACGAAACC TACGATGTGG CAGCGGACTC 4671

TTACAACGGT TATAACGACG CTGCCGAAAC CAGTTCCCGC CGGAGACAGC GCAACCATAC 4731

GCCGACTGCC AGTATTGAAC CGGTTAGTAC GGCCAGCAAT GTGATTGGCT TGCCGGTCTG 4791

AGCAGCAGCT CAGAAGTGGT GGTAATGGAA CCCGCTCTTT CGAAGAAATG CCCAGGCCAT 4851

TCAGGCTTTG ACGCGAACGC AAGACGATCG TGCTGAACCT GACGATGATG GAGCTGACAG 4911

CACAGGCGCG TCGATTT 4928

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 411 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Val Phe Asp Ala Leu Val Ile Gly Ser Gly Pro Ala Gly Leu Ala Ile
 1               5                  10                  15

Ala Ala Glu Leu Ala Gln Arg Gly Leu Lys Val Gln Gly Leu Ser Pro
            20                  25                  30

Val Asp Pro Phe His Pro Trp Glu Asn Thr Tyr Gly Ile Trp Gly Pro
        35                  40                  45

Glu Leu Asp Ser Leu Gly Leu Glu His Leu Phe Gly His Arg Trp Ser
    50                  55                  60

Asn Cys Val Ser Tyr Phe Gly Glu Ala Pro Val Gln His Gln Tyr Asn
65                  70                  75                  80

Tyr Gly Leu Phe Asp Arg Ala Gln Leu Gln Gln His Trp Leu Arg Gln
                85                  90                  95

Cys Glu Gln Gly Gly Leu Gln Trp Gln Leu Gly Lys Ala Ala Ala Ile
            100                 105                 110

Ala His Asp Ser His His Ser Cys Val Thr Thr Ala Ala Gly Gln Glu
        115                 120                 125
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Leu Gln Ala Arg Leu Val Val Asp Thr Thr Gly His Gln Ala Ala Phe
130 135 140

Ile Gln Arg Pro His Ser Asp Ala Ile Ala Tyr Gln Ala Ala Tyr Gly
145 150 155 160

Ile Ile Gly Gln Phe Ser Gln Pro Pro Ile Glu Pro His Gln Phe Val
165 170 175

Leu Met Asp Tyr Arg Ser Asp His Leu Ser Pro Glu Glu Arg Gln Leu
180 185 190

Pro Pro Thr Phe Leu Tyr Ala Met Asp Leu Gly Asn Asp Val Tyr Phe
195 200 205

Val Glu Glu Thr Ser Leu Ala Ala Cys Pro Ala Ile Pro Tyr Asp Arg
210 215 220

Leu Lys Gln Arg Leu Tyr Gln Arg Leu Ala Thr Arg Gly Val Thr Val
225 230 235 240

Gln Val Ile Gln His Glu Glu Tyr Cys Leu Phe Pro Met Asn Leu Pro
245 250 255

Leu Pro Asp Leu Thr Gln Ser Val Val Gly Phe Gly Gly Ala Ala Ser
260 265 270

Met Val His Pro Ala Ser Gly Tyr Met Val Gly Ala Leu Leu Arg Arg
275 280 285

Ala Pro Asp Leu Ala Asn Ala Ile Ala Ala Gly Leu Asn Ala Ser Ser
290 295 300

Ser Leu Thr Thr Ala Glu Leu Ala Thr Gln Ala Trp Arg Gly Leu Trp
305 310 315 320

Pro Thr Glu Lys Ile Arg Lys His Tyr Ile Tyr Gln Phe Gly Leu Glu
325 330 335

Lys Leu Met Arg Phe Ser Glu Ala Gln Leu Asn His His Phe Gln Thr
340 345 350

Phe Phe Gly Leu Pro Lys Glu Gln Trp Tyr Gly Phe Leu Thr Asn Thr
355 360 365

Leu Ser Leu Pro Glu Leu Ile Gln Ala Met Leu Arg Leu Phe Ala Gln
370 375 380

Ala Pro Asn Asp Val Arg Trp Gly Leu Met Glu Gln Gln Gly Arg Glu
385 390 395 400

Leu Gln Leu Phe Trp Gln Ala Ile Ala Ala Arg
405 410

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Asp Ala Leu Val Ile Gly Ser Gly Pro Ala Gly Leu Ala Ile Ala Ala
1 5 10 15

Glu Leu Ala Gln Arg Gly Leu Lys Val Gln Gly Leu Ser
20 25

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1614 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Nicotiana tabacum
(B) STRAIN: cv. xanthii
(F) TISSUE TYPE: Leaf

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

GGAACTTTCT TGAAATCCTG TTTGTAGTTT TCAAAAAAAA TTGAACCCCT GTTGGAAGAT 60

ATGGATACAT TGTTGAAAAC CCCAAATAAG CTTGAGTTTC TGCACCCAGT TCATGGATTT 120

TCTGTTAAAG CTAGCTCCTT TAACTCTGTA AAGCCCCATA AGTTTGGTTC TAGGAAAATT 180

TGTGAAAATT GGGGTAAAGG GGTTTGTGTT AAGGCTAAGA GTAGTGCCCT TTTGGAGCTT 240

GTACCTGAGA CCAAAAAGGA AAATCTTGAT TTTGAGCTTC CTATGTATGA CCCTTCAAAA 300

GGTCTTGTTG TAGATCTAGC TGTGGTTGGT GGTGGACCCG CTGGACTTGC AGTTGCACAG 360

CAGGTTTCGG AGGCTGGACT ATCGGTTGTT TCAATCGATC CATCGCCGAA ATTGATATGG 420

CCCAATAACT ATGGTGTTTG GGTGGATGAA TTTGAGGCCA TGGATTTGTT GGATTGCCTC 480

GACGCCACAT GGTCAGGTAC TGTTGTTTAT ATTGATGACA ATACAACTAA AGATCTTGAT 540

AGACCTTATG GAAGGGTTAA TCGGAAACAA CTTAAGTCCA AAATGATGCA GAAATGCATA 600

CTAAACGGTG TTAAATTCCA CCACGCCAAA GTTATAAAGG TAATTCACGA GGAAGCTAAA 660

TCTATGCTGA TTTGCAATGA TGGTGTAACT ATTCAGGCAA CGGTGGTGCT TGATGCAACT 720

GGCTTCTCAA GATGTCTTGT TCAGTATGAT AAGCCATATA AACCTGGATA TCAAGTAGCT 780

TATGGCATAT TGGCAGAAGT GGAGGAACAT CCCTTTGATA CAAGTAAGAT GGTTCTCATG 840

GATTGGCGAG ATTCGCATCT TGGTAATAAT ATGGAGCTGA AGGAGAGAAA TAGAAAAGTT 900

CCAACTTTTT TGTATGCCAT GCCATTTTCA TCAAATAAAA TATTTCTTGA AGAAACCTCA 960

CTTGTTGCTC GTCCTGGATT ACGTATGGAC GATATTCAAG AAAGAATGGT GGCTCGTTTA 1020

AATCACTTGG GTATAAAAGT TAAGAGCATT GAAGAGGACG AGCATTGTGT AATTCCGATG 1080

GGAGGCTCCC TTCCTGTAAT ACCTCAGAGA GTTGTTGGAA CTGGTGGTAC AGCTGGTCTG 1140

GTTCATCCCT CAACAGGTTA TATGGTAGCA AGGACCCTAG CTGCAGCTCC GGTCGTCGCT 1200

AATGCAATAA TTCACTACCT TGGTTCTGAG AAAGACCTTT TAGGTAATGA GTTATCTGCA 1260

GCTGTTTGGA AAGATTTGTG GCCCATAGAA AGGAGACGTC AACGAGAGTT CTTTTGTTTC 1320

GGTATGGATA TTCTTCTGAA GCTTGATTTA CCCGCTACAA GAAGGTTTTT CGATGCCTTT 1380

TTTGATCTAG AACCTCGTTA TTGGCATGGC TTCTTGTCAT CTCGCCTGTA TCTTCCTGAG 1440

CTTATATTTT TCGGGCTGTC CCTTTTCTCT CGCGCTTCAA ATACTTCTAG AATAGAGATT 1500

ATGACAAAGG GAACTCTTCC TTTGGTAAAT ATGATCAACA ATTTGTTACA GGATACAGAA 1560

TGACTTACCA GGAATCTTGT TCAATATTAC ATAGCATGTG TTAATACACT GCTC 1614

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1650 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Lycopersicon esculentum
(B) STRAIN: cv. VF36
(F) TISSUE TYPE: Leaf

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

GGCACGAGGA AACTTTTCTC TCTTCACTAG CTGTTTACAT GCTTGAAATT TCAAGATTTT 60

AGGACCCCAT TTGAAGTTTT CTTGAAACAA ATATTACCCT GTTGGAAAAA GATGGATACT 120

TTGTTGAAAA CCCCAAATAA CCTTGAATTT CTGAACCCAC ATCATGGTTT TGCTGTTAAA 180

GCTAGTACCT TTAGATCTGA GAAGCATCAT AATTTTGGTT CTAGGAAGTT TTGTGAAACT 240

TTGGGTAGAA GTGTTTGTGT TAAGGGTAGT AGTAGTGCTC TTTTAGAGCT TGTACCTGAG 300

ACCAAAAAGG AGAATCTTGA TTTTGAGCTT CCTATCTATG ACCCTTCAAA AGGGGTTGTT 360

GTGGATCTTG CTGTGGTTGG TGGTGGCCCT GCAGGACTTG CTGTTGCACA GCAAGTTTCT 420

GAAGCAGGAC TCTCTGTTTG TTCAATTGAT CCGAATCCTA AATTGATATG GCCTAATAAC 480

TATGGTGTTT GGGTGGATGA ATTTGAGGCT ATGGACTTGT TAGATTGTCT AGATGCTACC 540

TGGTCTGGTG CAGCAGTGTA CATTGATGAT AATACGGCTA AAGATCTTCA TAGACCTTAT 600

GGAAGGGTTA ACCGGAAACA GCTGAAATCG AAAATGATGC AGAAATGTAT AATGAATGGT 660

GTTAAATTCC ACCAAGCCAA AGTTATAAAG GTGATTCATG AGGAATCGAA ATCCATGTTG 720

ATATGCAATG ATGGTATTAC TATTCAGGCA ACGGTGGTGC TCGATGCAAC TGGCTTCTCT 780

AGATCTCTTG TTCAGTATGA TAAGCCTTAT AACCCCGGGT ATCAAGTTGC TTATGGCATT 840

TTGGCTGAAG TGGAAGAGCA CCCCTTTGAT GTAAACAAGA TGGTTTTCAT GGATTGGCGA 900

GATTCTCATT TGAAGAACAA TACTGATCTC AAGGAGAGAA ATAGTAGAAT ACCAACTTTT 960

CTTTATGCAA TGCCATTTTC ATCCAACAGG ATATTTCTTG AAGAAACATC ACTCGTAGCT 1020

CGTCCTGGCT TGCGTATAGA TGATATTCAA GAACGAATGG TGGCTCGTTT AAACCATTTG 1080

GGGATAAAAG TGAAGAGCAT TGAAGAAGAT GAACATTGTC TAATACCAAT GGGTGGTCCA 1140

CTTCCAGTAT TACCTCAGAG AGTCGTTGGA ATCGGTGGTA CAGCTGGCAT GGTTCATCCA 1200

TCCACCGGTT ATATGGTGGC AAGGACACTA GCTGCGGCTC CTGTTGTTGC CAATGCCATA 1260

ATTCAATACC TCGGTTCTGA AAGAAGTCAT TCGGGTAATG AATTATCCAC AGCTGTTTGG 1320

AAAGATTTGT GGCCTATAGA GAGGAGACGT CAAAGAGAGT TCTTCTGCTT CGGTATGGAT 1380

ATTCTTCTGA AGCTTGATTT ACCTGCTACA AGAAGGTTCT TTGATGCATT CTTTGACTTA 1440

GAACCTCGTT ATTGGCATGG CTTCTTATCG TCTCGATTGT TTCTACCTGA ACTCATAGTT 1500

TTTGGGCTGT CTCTATTCTC TCATGCTTCA AATACTTCTA GATTTGAGAT AATGACAAAG 1560

GGAACTGTTC CATTAGTAAA TATGATCAAC AATTTGTTAC AGGATAAAGA ATGAATCCGA 1620

GTAATTCGGA ATCTTGTCCA ATCTCGTGCC 1650

CLAIMS

1. A purified, isolated and cloned DNA sequence, designated *lcy* or *crtL*, for lycopene cyclase.

2. A DNA sequence as set forth in claim 1 selected from the group consisting of SEQ ID No:1 (bp2029-3261), SEQ ID No:4 and SEQ ID No:5.

3. An *E. coli* transformed with the DNA sequence for lycopene cyclase as set forth in claim 1.

4. A vector which comprises the DNA of claim 1.

5. A host cell, wherein the host cell is selected from the group of eucaryotic and procaryotic cells, which can be transformed with the vector of claim 4.

6. The host cell of claim 5 wherein it is *E. coli*.

7. The host cell of claim 5 wherein it is a cyanobacteria.

8. The host cell of claim 7 wherein it is selected from the group comprising *Synechococcus* PCC7942 and *Synechocystis* PCC6803.

9. The host cell of claim 5 wherein it is an alga.

10. The host cell of claim 5 wherein it is a plant cell.

11. The method of expressing the biosynthetic pathway from geranylgeranyl pyrophosphate to β-carotene

by incorporating the genes encoding the enzymes controlling the pathway in a host cell.

12. The method of claim 11 further characterized by including the steps of:

incorporating the DNA sequences encoding phytoene synthase, designated *psy*; phytoene desaturase, designated *pds*; ζ-carotene desaturase, designated *zds*; and lycopene cyclase, designated *lcy*.

13. The method of claim 11 further characterized by including the steps of

incorporating the DNA sequences encoding for phytoene synthase, designated *psy*; for phytoene desaturase in *Erwinia*, designated *crtI*; and for lycopene cyclase, originally designated *lcy*.

14. The method of claim 11 wherein the host cell is *E. coli*.

15. A purified, isolated and cloned DNA sequence comprising a nucleotide sequence for *lcy* which encodes a LCY polypeptide and at least one flanking DNA sequence.

16. A purified, isolated and cloned DNA sequence as set forth in claim 15 wherein the flanking DNA sequence is a promoter.

17. The DNA sequence of claim 15 wherein the nucleotide sequence for *lcy* is selected from the group consisting of SEQ ID No:1 (bp2029-3261), SEQ ID No:4 and SEQ ID No:5.

18. A vector which comprises the DNA of claim 15.

19. A host cell, wherein the host cell is selected from the group of eucaryotic and procaryotic cells which can be transformed with the vector of claim 18.

20. The host cell of claim 19 wherein it is *E. coli*.

21. The host cell of claim 19 wherein it is a cyanobacteria.

22. The host cell of claim 21 wherein it is selected from the group comprising *Synechococcus* PCC7942 and *Synechocystis* PCC6803.

23. The host cell of claim 19 wherein it is an alga.

24. The host cell of claim 19 wherein it is a plant cell.

25. A transgenic organism wherein the *lcy* DNA sequence is incorporated into the genomic DNA thereby producing lycopene cyclase and β-carotene.

26. The process of controlling carotenoid biosynthesis, content, composition or amount in bacteria, algae, and plants by

preparing vectors of a DNA sequence consisting of a purified, isolated and cloned DNA sequence comprising a nucleotide sequence for *lcy* which encodes a LCY polypeptide and at least one flanking DNA sequence; and

inserting said vectors in the cells of bacteria, algae and plants thereby forming transgenic organisms.

27. The process of claim 26 wherein the vector consists of the *lcy* DNA sequence and a promoter.

28. A purified, isolated and cloned DNA sequence consisting of a modified DNA sequence encoding lycopene cyclase that is resistant to herbicides.

29. A modified DNA sequence as set forth in Claim 28 further characterized by said resistance including resistance to bleaching herbicides of the trialkylamine family including CPTA and MPTA.

30. A transformed *E. coli* carrying the DNA sequence for lycopene cyclase as set forth in claim 28.

31. A transformed *E. coli* as set forth in claim 30 further characterized by said resistance including resistance to bleaching herbicides of the trialkylamine family including CPTA and MPTA.

32. A vector which comprises the DNA of claim 28.

33. A host cell, wherein the host cell is selected from the group of eucaryotic and procaryotic cells which can be transformed with the vector of claim 32.

34. The host cell of claim 33 wherein it is *E. coli*.

35. The host cell of claim 33 wherein it is a cyanobacteria.

36. The host cell of claim 35 wherein it is selected from the group comprising *Synechococcus* PCC7942 and *Synechocystis* PCC6803.

37. The host cell of claim 33 wherein it is an alga.

38. The host cell of claim 33 wherein it is a plant cell.

39. A vector which comprises the DNA of claim 29.

40. A host cell, wherein the host cell is selected from the group of eucaryotic and procaryotic cells which can be transformed with the vector of claim 39.

41. The host cell of claim 40 wherein it is *E. coli*.

42. The host cell of claim 40 wherein it is a cyanobacteria.

43. The host cell of claim 42 wherein it is selected from the group comprising *Synechococcus* PCC7942 and *Synechocystis* PCC6803.

44. The host cell of claim 40 wherein it is an alga.

45. The host cell of claim 40 wherein it is a plant cell.

46. A purified, isolated and cloned DNA sequence comprising a nucleotide sequence for *lcy* which encodes a LCY polypeptide and at least one flanking DNA sequence characterized by point mutations, deletions or insertions such that the resulting sequence is altered imparting herbicide resistance.

47. The DNA sequence of claim 46 further characterized by point mutations, deletions or insertions occurring within the nucleotide sequence of *lcy* such that the resulting amino acid sequence is altered imparting herbicide resistance.

48. The DNA sequence of claim 46 further characterized by the point mutations, deletions or insertions occurring within the flanking sequences of *lcy* such that regulation of *lcy* is altered imparting herbicide-resistance.

49. The DNA sequence of claim 48 wherein the flanking sequence is a promoter.

50. The DNA sequence as set forth in claim 48 further characterized by a change in the sequence from C to T at base 1925 of SEQ ID No:1.

51. The DNA sequence of claim 46 further characterized by being an effective fragment of the sequence encompassing the point mutation, deletions or insertions.

52. A vector which comprises the DNA of claim 46.

53. A host cell, wherein the host cell is selected from the group of eucaryotic and procaryotic cells, which can be transformed with the vector of claim 52.

54. The host cell of claim 53 wherein it is *E. coli*.

55. The host cell of claim 53 wherein it is a cyanobacteria.

56. The host cell of claim 55 wherein it is selected from the group comprising *Synechococcus* PCC7942 and *Synechocystis* PCC6803.

57. The host cell of claim 53 wherein it is an alga.

58. The host cell of claim 53 wherein it is a plant cell.

59. A transgenic organism wherein the DNA sequence as set forth in claim 28 is incorporated into the genomic DNA thereby producing an herbicide-resistant organism.

60. A transgenic organism wherein the DNA sequence as set forth in claim 46 is incorporated into the genomic DNA thereby producing an herbicide-resistant organism.

61. A transgenic organism wherein the DNA sequence as set forth in claim 29 is incorporated into the genomic DNA thereby producing an organism resistant to bleaching herbicides of the trialkylamine family including CPTA and MPTA.

62. A transgenic organism wherein the DNA sequence as set forth in claim 47 is incorporated into the genomic DNA thereby producing an herbicide-resistant organism.

63. A transgenic organism wherein the DNA sequence as set forth in claim 48 is incorporated into the genomic DNA thereby producing an herbicide-resistant organism.

64. A transgenic organism wherein the DNA sequence as set forth in claim 50 is incorporated into the genomic DNA thereby producing an herbicide-resistant organism.

65. The process of controlling carotenoid biosynthesis, content, composition or amount in bacteria, algae, and plants by

preparing vectors of a DNA sequence consisting of a purified, isolated and cloned DNA sequence comprising a nucleotide sequence for *lcy* which encodes a LCY polypeptide and at least one flanking DNA sequence characterized by point mutations, deletions or insertions in the DNA sequence such that the resulting sequence is altered imparting herbicide resistance; and

inserting said vectors in the cells of bacteria, algae and plants thereby forming transgenic organisms.

66. The process of claim 65 wherein the point mutations, deletions or insertions occur within the nucleotide sequence of *lcy* such that the resulting amino acid sequence is altered imparting herbicide resistance.

67. The process of claim 65 wherein the point mutations, deletions or insertions occur within the flanking sequences of *lcy* such that regulation of *lcy* is altered imparting herbicide-resistance.

68. A plasmid designated pLYCB-M5XE.

69. A process of construction of plants or algae that are resistant to the action of herbicides which interact with the lycopene cyclase enzyme by

screening cyanobacteria for a clone resistant to a herbicide,

purifying and isolating an altered DNA sequence controlling production of a herbicide resistant lycopene cyclase enzyme,

determining the modification of the DNA sequence needed for production of the herbicide resistant enzyme, and

altering the plant or algae to produce an analogous modification in the native plant or algae DNA sequence.

70. A transgenic organism wherein the anti-sense expression of the *lcy* DNA sequence is incorporated into the genomic DNA thereby inhibiting the synthesis of lycopene cyclase and accumulating the red pigment lycopene.

71. The process of controlling carotenoid biosynthesis, content, composition or amount in bacteria, algae, and plants by

preparing vectors of a DNA sequence consisting of an anti-sense expression of the *lcy* DNA sequence; and

inserting said vectors in the cells of bacteria, algae and plants thereby forming transgenic organisms.

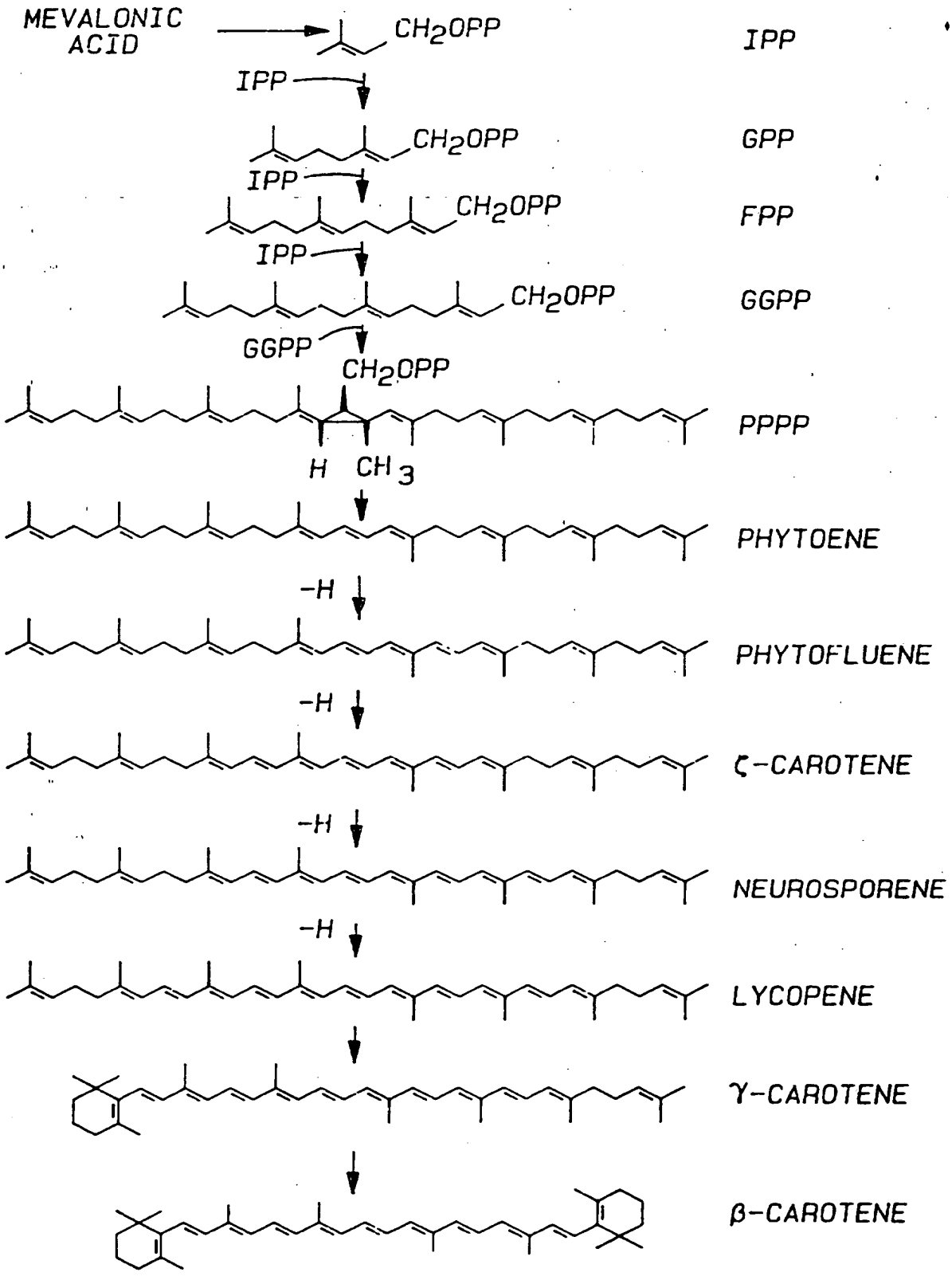
MEVALONIC ACID
CH_2OPP
IPP
IPP
CH_2OPP
GPP
IPP
CH_2OPP
FPP
IPP
CH_2OPP
GGPP
GGPP
CH_2OPP
PPPP
H CH_3
PHYTOENE
-H
PHYTOFLUENE
-H
ζ-CAROTENE
-H
NEUROSPORENE
-H
LYCOPENE
γ-CAROTENE
β-CAROTENE

Fig-1

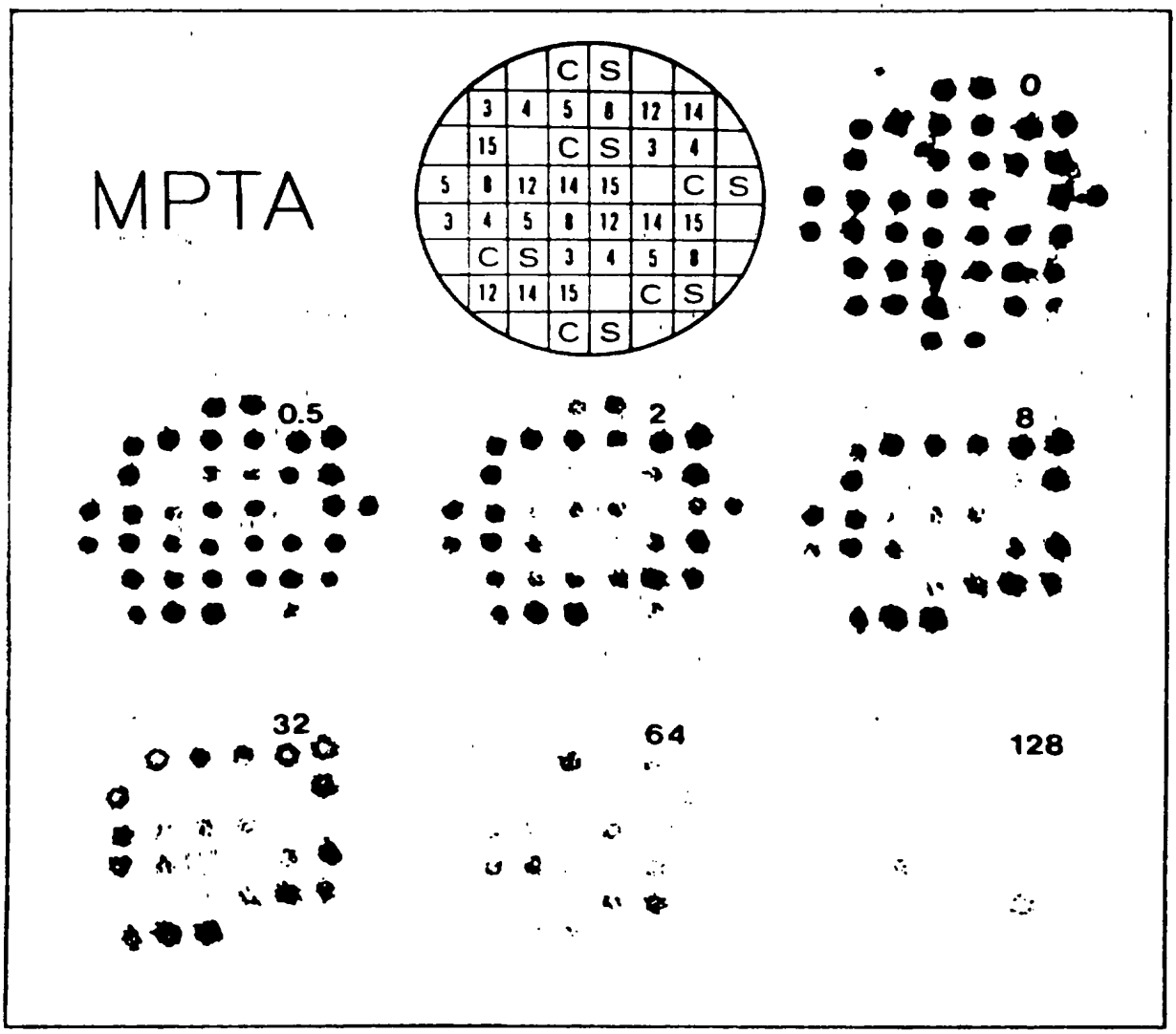

Fig-2

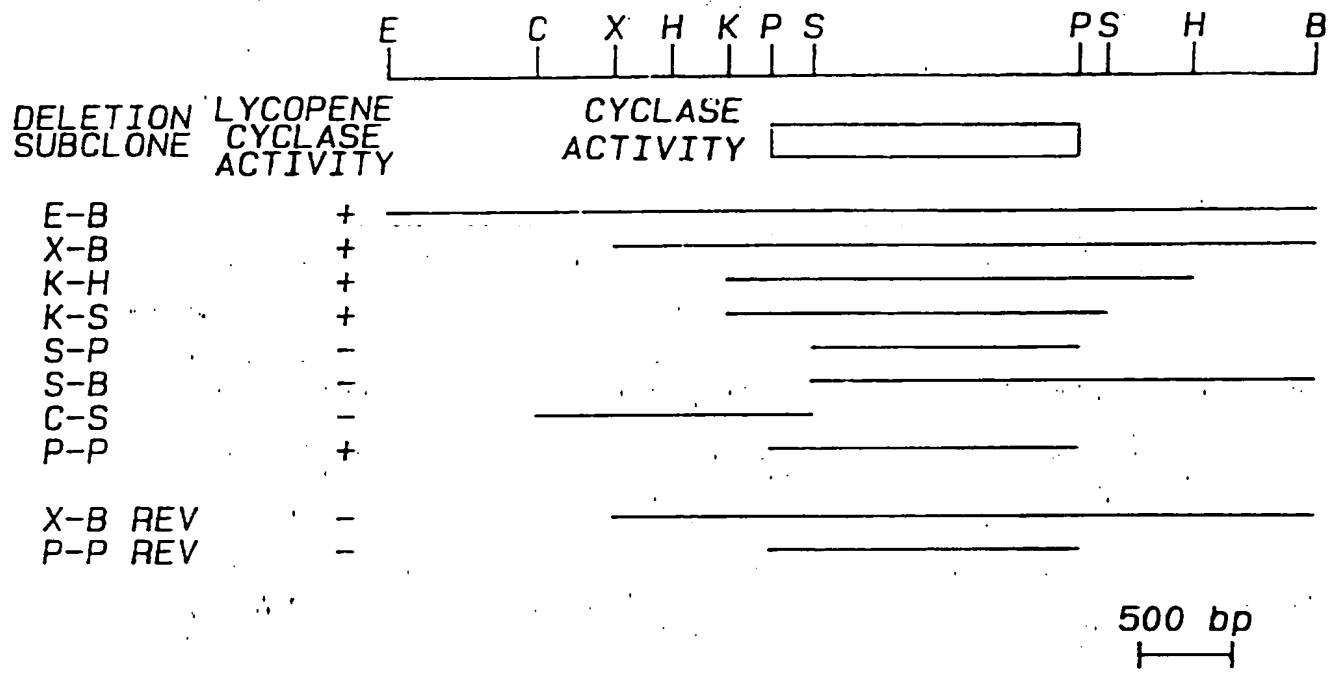
E C X H K P S P S H B
DELETION SUBCLONE
LYCOPENE CYCLASE ACTIVITY
CYCLASE ACTIVITY
E-B +
X-B +
K-H +
K-S +
S-P –
S-B –
C-S –
P-P +
X-B REV –
P-P REV –
500 bp

Fig-3

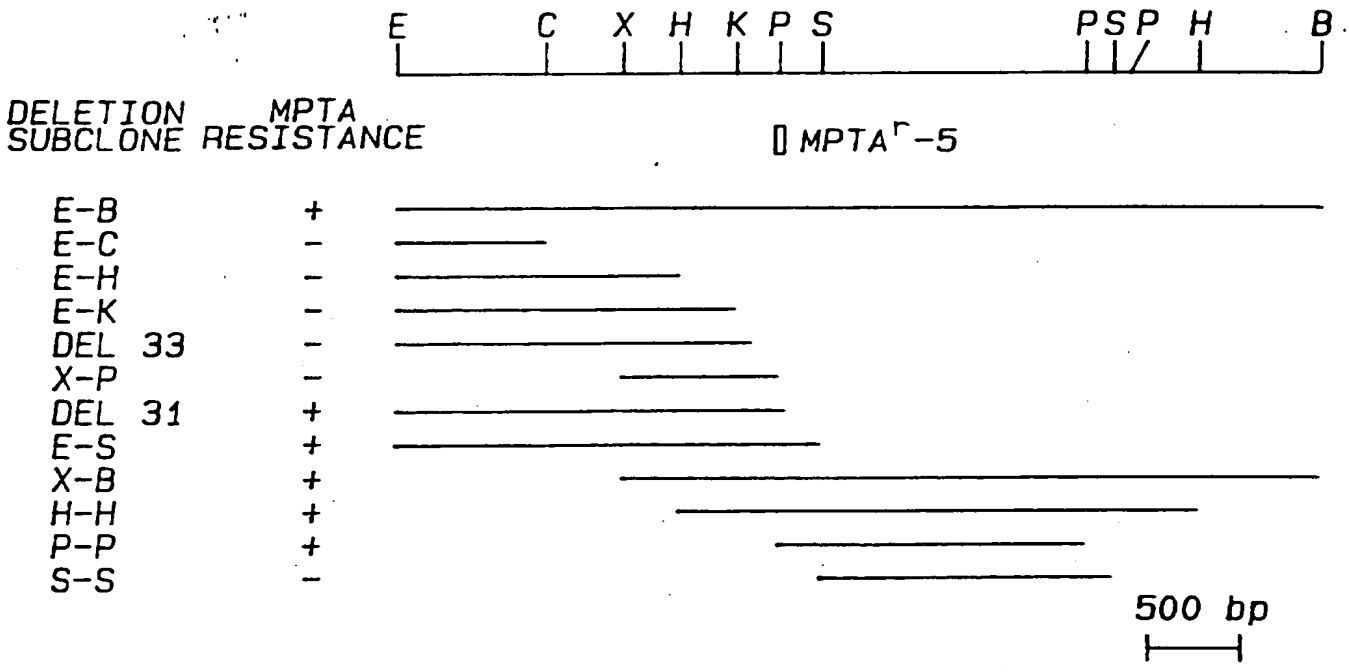
E C X H K P S P S P H B
DELETION SUBCLONE
MPTA RESISTANCE
MPTA^r-5
E-B +
E-C –
E-H –
E-K –
DEL 33 –
X-P –
DEL 31 +
E-S +
X-B +
H-H +
P-P +
S-S –
500 bp

Fig-4

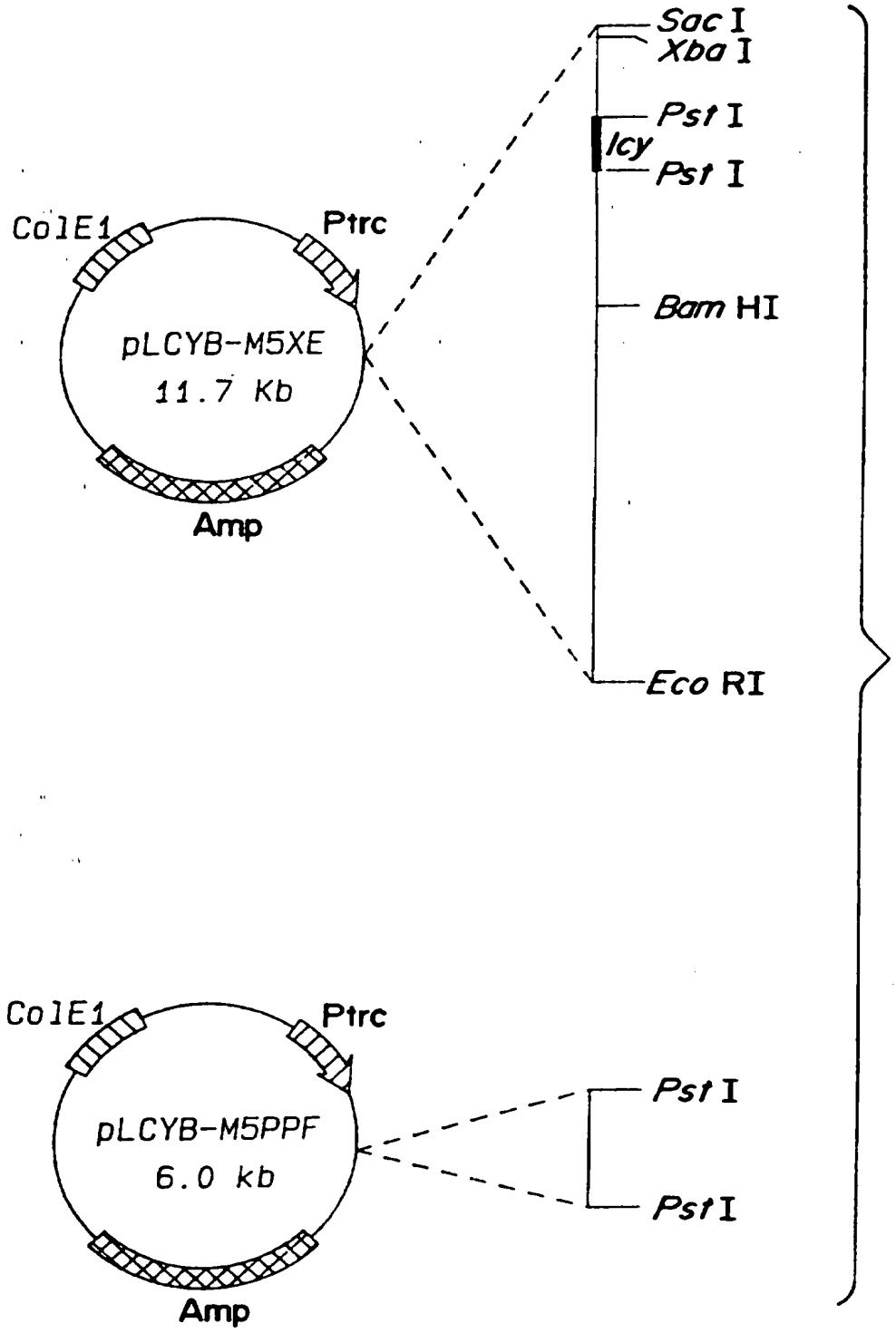
Sac I
Xba I
Pst I
lcy
Pst I
Bam HI
Eco RI
ColE1
Ptrc
pLCYB-M5XE
11.7 Kb
Amp
ColE1
Ptrc
pLCYB-M5PPF
6.0 kb
Amp
Pst I
Pst I

Fig-5

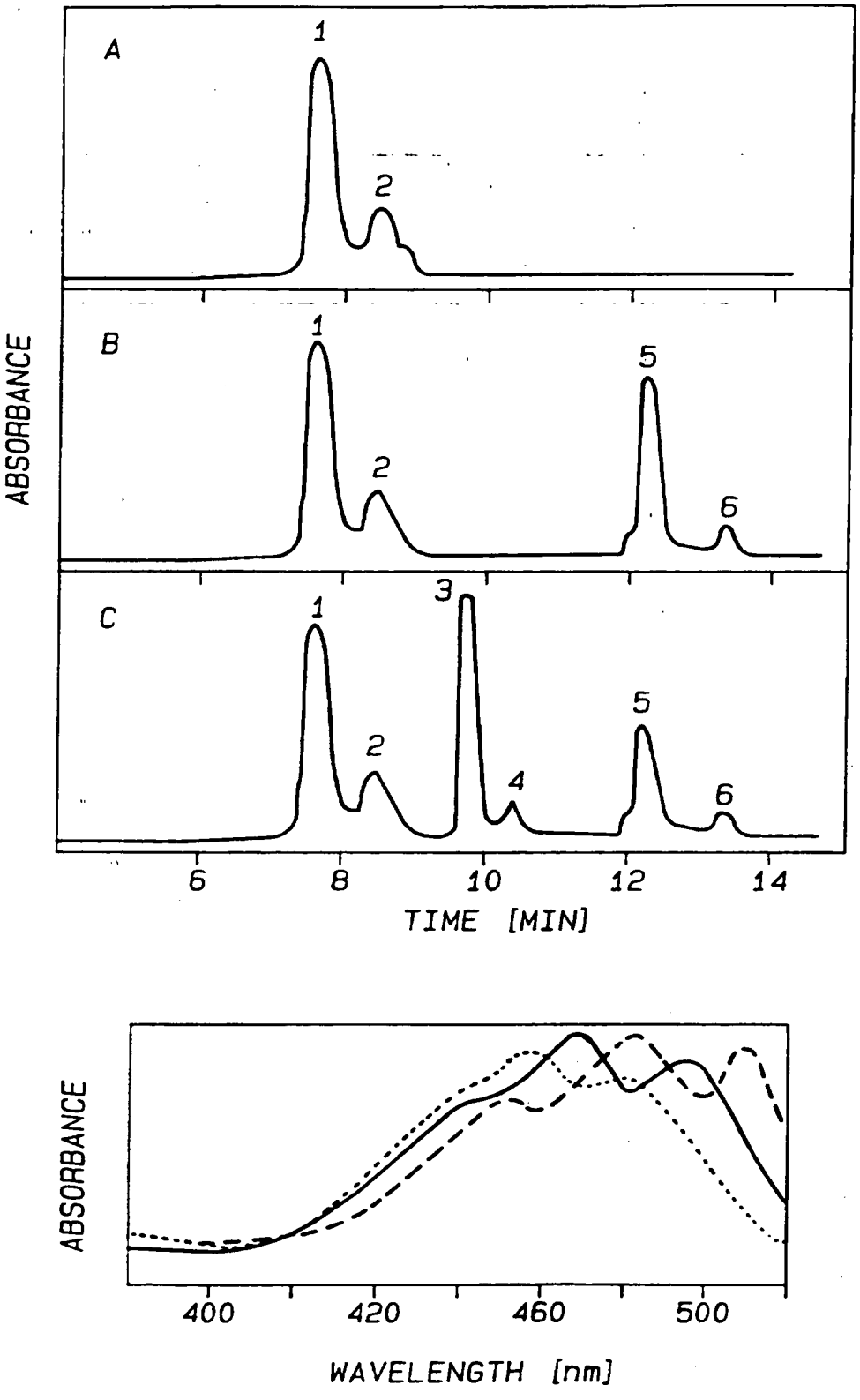
A
B
C
1
2
3
4
5
6
ABSORBANCE
6
8
10
12
14
TIME [MIN]
ABSORBANCE
400
420
460
500
WAVELENGTH [nm]

Fig-6

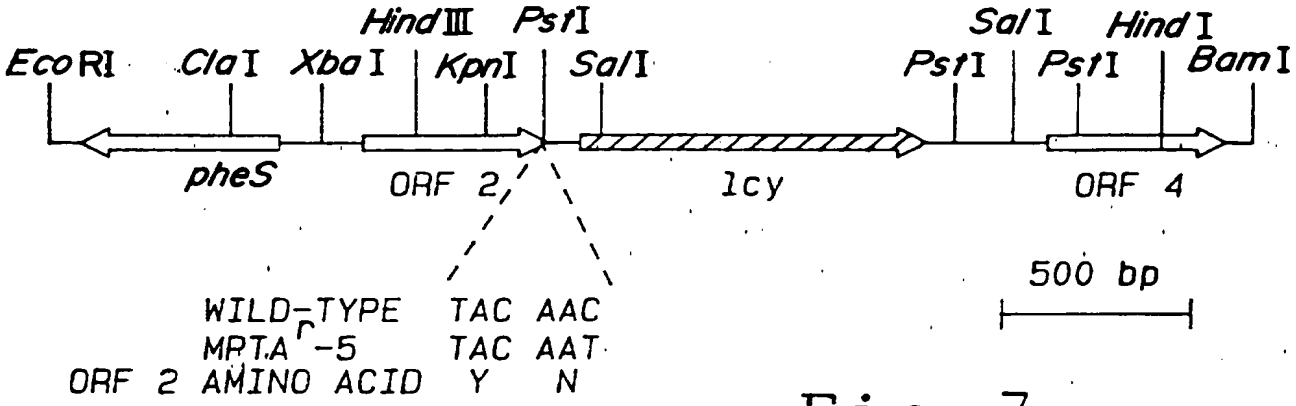

Fig-7

```
                                  A  A                              S
FAD CONSENSUS:          pssssGGG*GGs**s**s******s*ssa
                        |||||||| |||  |  |       | |||
lcy GENE PRODUCT:       DALVIGSGPAGLAIAAELAQRGLKVQGLS
```

Fig-8

INTERNATIONAL SEARCH REPORT

International application No.
PCT/US96/03044

A. CLASSIFICATION OF SUBJECT MATTER
IPC(6) :A01H 5/00, 13/00; C12N 15/09, 15/29, 15/52, 15/63, 15/82
US CL :800/205; 435/69.1, 172.1, 172.3, 240.4, 252.3
According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)
U.S. : 800/205; 435/69.1, 172.1, 172.3, 240.4, 252.3

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
APS, DIALOG

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	MISAWA et al. Elucidation of the Erwinia uredovora Carotenoid Biosynthetic Pathway by Functional Analysis of Gene Products Expressed in E. coli. J. Bacteriol. December 1990, Vol. 172, No. 12, pages 6704-6712, especially page 6704.	1-71
Y	CHAMOVITZ et al. The molecular basis of resistance to the herbicide norflurazon. Plant Molecular Biology. 1991, Vol. 16, pages 967-974, especially page 970.	28-69
Y	SANDMANN et al. Herbicides affecting plant pigments. 1987 British Crop Protection Conference - Weeds. November 1987, pages 139-148, see page 139.	28-69

[X] Further documents are listed in the continuation of Box C. [ ] See patent family annex.

* Special categories of cited documents:
"A" document defining the general state of the art which is not considered to be of particular relevance
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"O" document referring to an oral disclosure, use, exhibition or other means
"P" document published prior to the international filing date but later than the priority date claimed
"T" later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
"X" document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
"Y" document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
"&" document member of the same patent family

Date of the actual completion of the international search
13 JUNE 1996

Date of mailing of the international search report
10 JUL 1996

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C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BIRD et al. Using antisense RNA to study gene function: inhibition of carotenoid biosynthesis in transgenic tomatoes. BIO/TECHNOLOGY. July 1991, Vol. 9, pages 635-639, especially page 637.	70-71